In the Specification:

Please delete the section on page 1, lines 5 to 7, entitled "STATEMENT OF GOVERNMENT SUPPORT".

Please amend the paragraph beginning at page 9, line 7 of the specification as follows:

--Figures ~~1A-1H~~ 1A-1H and Figure 2 are representative consensus diagrams that show examples of conserved regions from 16S rRNA (Fig. ~~1A-1B~~ 1A-1, 1A-2, 1A-3, 1A-4, and 1A-5), 23S rRNA (3'-half, Fig. ~~1C-1D~~ 1B, 1C, and 1D; 5'-half, Fig. 1E-F), 23S rRNA Domain I (Fig. 1G), 23S rRNA Domain IV (Fig. 1H) and 16S rRNA Domain III (Fig. ~~1~~ 2) which are suitable for use in the present invention. Lines with arrows are examples of regions to which intelligent primer pairs for PCR are designed. The label for each primer pair represents the starting and ending base number of the amplified region on the consensus diagram. Bases in capital letters are greater than 95% conserved; bases in lower case letters are 90-95% conserved, filled circles are 80-90% conserved; and open circles are less than 80% conserved. The label for each primer pair represents the starting and ending base number of the amplified region on the consensus diagram. The nucleotide sequence of the 16S rRNA consensus sequence is SEQ ID NO:3 and the nucleotide sequence of the 23S rRNA consensus sequence is SEQ ID NO:4.--

Please amend the paragraph beginning at page 9, line 17 of the specification as follows:

--Figure 2 shows a typical primer amplified region from the 16S rRNA Domain III shown in Figure ~~1C~~ 1A-1.--

Please amend the paragraph beginning at page 13, line 4 of the specification as follows:

--As used herein, "intelligent primers" are primers which bind to sequence regions which flank an intervening variable region. In a preferred embodiment, these sequence regions which flank the variable region are highly conserved among different species of bioagent. For example, the sequence regions may be highly conserved among all Bacillus species. By the term "highly conserved," it is meant that the sequence regions exhibit between about 80-100%, more preferably

between about 90-100% and most preferably between about 95-100% identity. Examples of intelligent primers which amplify regions of the 16S and 23S rRNA are shown in Figures ~~1A-1H~~ 1A-1H. A typical primer amplified region in 16S rRNA is shown in Figure 2. The arrows represent primers which bind to highly conserved regions which flank a variable region in 16S rRNA domain III. The amplified region is the stem-loop structure under "1100-1188."--

B2

Please amend the paragraph beginning at page 23, line 21 of the specification as follows:

B3

--The method of the present invention can also be used for blood typing. The gene encoding A, B or O blood type can differ by four single nucleotide polymorphisms. If the gene contains the sequence CGTGGTGACCCTT ~~(SEQ ID NO:1)~~ (SEQ ID NO:5), antigen A results. If the gene contains the sequence CGTCGTCACCGCTA ~~(SEQ ID NO:2)~~ (SEQ ID NO:6) antigen B results. If the gene contains the sequence CGTGGT-ACCCCTT ~~(SEQ ID NO:3)~~ (SEQ ID NO:7), blood group O results ("-" indicates a deletion). These sequences can be distinguished by designing a single primer pair which flanks these regions, followed by amplification and mass determination.--

Please amend the paragraph beginning at page 31, line 9 of the specification as follows:

B4

--*B.anthracis*_16S_971

GCGAAGAACCUUACCAGGU**M**UUGACAUCCUCUGA**C**AACCCUAGAGAUAGGGCUUCUC

CUUCGGGAGCAGAGUGACAGGUGGUGCAUGGUU ~~(SEQ ID NO:4)~~ (SEQ ID NO:1)--

Please amend the paragraph beginning at page 32, line 1 of the specification as follows:

B5

--*B.cereus*_16S_971

GCGAAGAACCUUACCAGGUCUUGACAUCCUCUGA**A**AACCCUAGAGAUAGGGCUUC

UCCUUCGGGAGCAGAGUGACAGGUGGUGCAUGGUU ~~(SEQ ID NO:5)~~ (SEQ ID NO:2)--